

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2006, 16:14:09 ; Search time 686 Seconds  
(without alignments)  
10776.605 Million cell updates/sec

Title: US-10-623-155-160

Perfect score: 3951

Sequence: 1 tctgcatccattgaaac.....taattaaaacataaaaaa 3951

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq:\*
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- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3951	100.0	3951	3	US-09-643-597-160 Sequence 160, App
2	3951	100.0	3951	3	US-09-480-884A-160 Sequence 160, App
3	3951	100.0	3951	3	US-09-542-615A-160 Sequence 160, App
4	3951	100.0	3951	3	US-09-606-421B-160 Sequence 160, App
5	3951	100.0	3951	3	US-09-221-107-160 Sequence 160, App
6	3951	100.0	3951	3	US-09-466-396A-160 Sequence 160, App
7	3951	100.0	3951	3	US-09-476-496A-160 Sequence 160, App
8	3951	100.0	3951	3	US-09-630-940B-160 Sequence 160, App
9	3951	100.0	3951	3	US-09-285-479-160 Sequence 160, App
10	3951	100.0	3951	3	US-10-007-700-160 Sequence 160, App
11	3616.4	91.5	3669	3	US-09-949-016-2224 Sequence 2224, App
12	3104.4	78.6	3156	3	US-09-919-172-86 Sequence 86, Appl
13	3101.2	78.5	3190	3	US-09-623-624-3 Sequence 3, Appl1
14	3101.2	78.5	3190	3	US-10-270-595-3 Sequence 3, Appl1
15	2930	74.2	2970	3	US-09-193-562D-31 Sequence 31, Appl
16	2930	74.2	2970	3	US-10-055-412B-31 Sequence 31, Appl
17	2800.8	70.9	3362	3	US-09-643-597-167 Sequence 167, App
18	2800.8	70.9	3362	3	US-09-480-884A-167 Sequence 167, App
19	2800.8	70.9	3362	3	US-09-542-615A-167 Sequence 167, App
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22	2800.8	70.9	3362	3	US-09-476-496A-167 Sequence 167, App
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24	2800.8	70.9	3362	3	US-09-285-479-167 Sequence 167, App
25	2800.8	70.9	3362	3	US-10-007-700-167 Sequence 167, App
26	2772	70.2	2784	3	US-09-643-597-168 Sequence 168, App
27	2772	70.2	2784	3	US-09-480-884A-168 Sequence 168, App
28	2772	70.2	2784	3	US-09-542-615A-168 Sequence 168, App
29	2772	70.2	2784	3	US-09-606-421B-168 Sequence 168, App
30	2772	70.2	2784	3	US-09-466-396A-168 Sequence 168, App
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32	2772	70.2	2784	3	US-09-630-940B-168 Sequence 168, App
33	2772	70.2	2784	3	US-09-285-479-168 Sequence 168, App
34	2772	70.2	2784	3	US-10-007-700-168 Sequence 168, App
35	2742.6	69.4	8031	3	US-09-643-597-254 Sequence 254, App
36	2742.6	69.4	8031	3	US-09-480-884A-254 Sequence 254, App
37	2742.6	69.4	8031	3	US-09-542-615A-254 Sequence 254, App
38	2742.6	69.4	8031	3	US-09-606-421B-254 Sequence 254, App
39	2742.6	69.4	8031	3	US-09-476-496A-254 Sequence 254, App
40	2742.6	69.4	8031	3	US-09-630-940B-254 Sequence 254, App
41	2742.6	69.4	8031	3	US-10-007-700-254 Sequence 254, App
42	2740.2	69.4	2773	3	US-09-643-597-358 Sequence 358, App
43	2740.2	69.4	2773	3	US-09-630-940B-358 Sequence 358, App
44	2740.2	69.4	2773	3	US-10-007-700-358 Sequence 358, App
45	2619	66.3	2646	3	US-10-007-700-431 Sequence 431, App

#### ALIGNMENTS

##### RESULT 1

US-09-643-597-160  
; Sequence 160, Application US/09643597  
; Patent No. 6426072  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C11  
; CURRENT APPLICATION NUMBER: US/09/643,597  
; CURRENT FILING DATE: 2000-08-21  
; NUMBER OF SEQ ID NOS: 369  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 160  
; LENGTH: 3951  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-643-597-160

Query Match 100.0%; Score 3951; DB 3; Length 3951;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GAGGCTTCTCTCAACATGACCAAGGAGCATTCGAGTCTTATTTGCAACTGAAGTT	120
DB	61	GAGGCTTCTCTCAACATGACCAAGGAGCATTCGAGTCTTATTTGCAACTGAAGTT	120
QY	121	TGTGACTCTCTGGTTCCTTAAGTTTCAAGTCCCATTCCTGGGAGCTGGAGTACAGCT	180
DB	121	TGTGACTCTCTGGTTCCTTAAGTTTCAAGTCCCATTCCTGGGAGCTGGAGTACAGCT	180
QY	181	TCAGACATGGGTATATGATTCCTCATTTATTCCTCAGGTACCTGAGATCA	240

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 18:05:02 : Search time 471 Seconds

(without alignments)  
6642.696 Million cell updates/sec

Title: US-10-623-155-161

Perfect score: 4942

Sequence: 1 MTQSIAGPICNLKVTLLV.....HHTLSKKRADKNGTKLL 943

Scoring table:

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 3380774 seqs, 1105942010 residues

Total number of hits satisfying chosen parameters: 6761548

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4942	100.0	3951	6	US-10-550-797-1
2	4939	99.9	2832	8	US-11-371-354-64288
3	4939	99.9	3669	6	US-10-533-069-578
4	4939	99.9	3955	1	PCT-US06-33148-1637
5	4939	99.9	3955	8	US-11-431-708-4126
6	4939	99.9	3955	8	US-11-475-062-7433
7	4939	99.9	4007	1	PCT-US06-33148-21
8	4939	99.9	4007	8	US-11-363-151-13

9	4939	99.9	4022	1	PCT-US06-33148-1639	Sequence 1639, Ap
10	1996	40.4	3350	8	US-11-475-062-9462	Sequence 9462, Ap
11	1993	40.3	3311	1	PCT-US06-33148-23	Sequence 23, Appl
12	1993	40.3	3311	8	US-11-475-062-9463	Sequence 9463, Ap
13	1993	40.3	3311	9	US-60-836-986-13328	Sequence 13328, A
14	1986	40.2	3340	1	PCT-US06-33148-1645	Sequence 1645, Ap
15	1985.5	40.2	2804	1	PCT-US06-33148-1649	Sequence 1649, Ap
16	1964.5	39.8	3218	9	US-60-836-986-13329	Sequence 13329, A
17	1932.5	39.1	3195	6	US-10-276-115A-22	Sequence 22, Appl
18	1927.5	39.0	4569	6	US-10-276-115A-3	Sequence 3, Appl
19	1817	36.8	2663	1	PCT-US06-33148-1647	Sequence 1647, Ap
20	1472	29.8	2144	1	PCT-US06-33148-1643	Sequence 1643, Ap
21	1472	29.8	2209	1	PCT-US06-33148-174	Sequence 174, App
22	772	15.6	451	8	US-11-290-215A-174	Sequence 3168, A
23	455.5	9.2	731	8	US-11-433-832-31627	Sequence 31627, A
24	234	4.7	2350	8	US-11-433-832-31627	Sequence 2831, Ap
25	175	3.5	421	6	US-10-664-025A-2831	Sequence 2685, Ap
26	159	3.2	4997	9	US-60-836-986-2685	Sequence 1008, Ap
27	147	3.0	4128	1	PCT-US06-33712-1008	Sequence 206, App
28	133.5	2.7	19341	9	US-60-836-986-206	Sequence 5, Appl
29	133	2.7	5658	7	US-11-332-464-5	Sequence 3, Appl
30	131.5	2.7	2808	6	US-10-587-052-3	Sequence 1, Appl
31	131	2.7	4623	9	PCT-US06-30281-11364	Sequence 11364, A
32	130.5	2.6	8192	1	PCT-US06-30281-11364	Sequence 757, App
33	130	2.6	4578	6	US-10-669-920-757	Sequence 1, Appl
34	130	2.6	330400	6	US-10-805-394A-1	Sequence 3, Appl
35	129.5	2.6	3842	1	PCT-US06-20645-3	Sequence 47364, A
36	129.5	2.6	3846	8	US-11-433-832-47364	Sequence 1, Appl
37	129.5	2.6	10011	1	PCT-US06-20645-1	Sequence 4370, Ap
38	129.5	2.6	10011	6	US-10-533-520-4370	Sequence 14427, A
39	129.5	2.6	10011	9	US-60-836-986-14427	Sequence 1, Appl
40	129	2.6	1983043	6	US-10-961-644A-1	Sequence 4220, Ap
41	126.5	2.6	4778	8	US-11-437-729-4220	Sequence 26834, A
42	126.5	2.6	4793	7	US-11-520-715-26834	Sequence 4219, Ap
43	126.5	2.6	4816	8	US-11-437-729-4219	Sequence 8389, Ap
44	126.5	2.6	4816	8	US-11-475-062-8389	Sequence 6349, Ap
45	126.5	2.6	4828	6	US-10-533-520-6349	

ALIGNMENTS

RESULT 1

US-10-550-797-1

; Sequence 1, Application US/10550797

; GENERAL INFORMATION:

; APPLICANT: Zehentner-Wilkinson, Barbara K.

; APPLICANT: Hayes, Dawn

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION

; TITLE OF INVENTION: AND MONITORING OF LUNG CANCER

; FILE REFERENCE: 210121.609USPC

; CURRENT APPLICATION NUMBER: US/10/550,797

; CURRENT FILING DATE: 2005-09-22

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 1

; LENGTH: 3951

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-550-797-1

Alignment Scores:

Pred. No.:

Score: 0

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 6

US-10-623-155-161 (1-943) x US-10-550-797-1 (1-3951)

QY 1 MetThrGlnArgSerIleAlaClyProIleCysAsnLeuLysPheValThrIleuVal 20

|||||

GenCore version 5.1.9  
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QM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 17:56:17 ; Search time 53208 Seconds  
 (without alignments)  
 1554.082 Million cell updates/sec

Title: US-10-623-155-161  
 Perfect score: 4942  
 Sequence: 1 WTQSRSTAGPICNLKFTLLV.....HTLSRKKRDKKENGTKLL 943

Scoring table: BLOSUM62  
 Xgapop 10.0, Xgapext 0.5  
 Ygapop 10.0, Ygapext 0.5  
 Fgapop 6.0, Fgapext 7.0  
 Delop 6.0, Delext 7.0

Searched: 86534536 seqs, 29229259966 residues

Total number of hits satisfying chosen parameters: 173069072

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 -THR MIN=0 -ALIGN=15 -NODES=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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62:	/EMC_Celerra_SIDS3/ptodata/2/pna/US109B_COMB.seq:
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65:	/EMC_Celerra_SIDS3/ptodata/2/pna/US110A_COMB.seq:
66:	/EMC_Celerra_SIDS3/ptodata/2/pna/US110B_COMB.seq:
67:	/EMC_Celerra_SIDS3/ptodata/2/pna/US110C_COMB.seq:
68:	/EMC_Celerra_SIDS3/ptodata/2/pna/US110D_COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	4942	100.0	1	PCT-US01-47576-160 Sequence 160, App
2	4942	100.0	3	PCT-US04-07451-1 Sequence 1, Appli
3	4942	100.0	3	PCT-US04-23085-160 Sequence 160, App
4	4942	100.0	24	US-Q9-510-376A-160 Sequence 160, App

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5 4942 100.0 3951 28 US-09-662-786-160 Sequence 160, App
6 4942 100.0 3951 28 US-09-685-696-160 Sequence 160, App
7 4942 100.0 3951 30 US-09-735-705-160 Sequence 160, App
8 4942 100.0 3951 32 US-09-850-716-160 Sequence 160, App
9 4942 100.0 3951 32 US-09-850-716-160 Sequence 160, App
10 4942 100.0 3951 33 US-09-897-778-160 Sequence 160, App
11 4942 100.0 3951 41 US-10-117-982-160 Sequence 160, App
12 4942 100.0 3951 48 US-10-313-986-160 Sequence 160, App
13 4942 100.0 3951 52 US-10-623-155-160 Sequence 160, App
14 4942 100.0 3951 60 US-10-775-972-160 Sequence 160, App
15 4942 100.0 3951 62 US-10-922-124-160 Sequence 160, App
16 4942 100.0 3951 74 US-11-392-479-1 Sequence 1, Appli
17 4939 99.9 2832 1 PCT-US03-01450-30 Sequence 30, Appl
18 4939 99.9 2832 49 US-10-345-680-30 Sequence 30, Appl
19 4939 99.9 2832 73 US-11-302-678-30 Sequence 28, Appl
20 4939 99.9 2970 1 PCT-US03-01450-28 Sequence 28, Appl
21 4939 99.9 2970 49 US-10-345-680-28 Sequence 31, Appl
22 4939 99.9 2970 60 US-10-779-949-31 Sequence 28, Appl
23 4939 99.9 2970 73 US-11-302-678-28 Sequence 1, Appli
24 4939 99.9 2970 82 US-60-414-262-1 Sequence 615, App
25 4939 99.9 3669 51 US-10-529-348-615 Sequence 70, Appl
26 4939 99.9 3671 1 PCT-US02-21338A-196 Sequence 196, App
27 4939 99.9 3671 1 PCT-US02-21338A-196 Sequence 196, App
28 4939 99.9 3671 41 US-10-126-052A-518 Sequence 518, App
29 4939 99.9 3671 41 US-10-188-832-196 Sequence 196, App
30 4939 99.9 3671 41 US-10-295-027-317 Sequence 317, App
31 4939 99.9 3671 43 US-10-295-027-317 Sequence 1025, App
32 4939 99.9 3671 63 US-10-952-698-196 Sequence 196, App
33 4939 99.9 3671 85 US-60-679-970-1190 Sequence 1190, App
34 4939 99.9 4007 74 US-11-363-149-13 Sequence 13, Appl
35 4939 99.9 4007 74 US-11-363-149-13 Sequence 13, Appl
36 4939 99.9 4007 85 US-60-679-970-1191 Sequence 1191, App
37 4939 99.9 4007 86 US-60-710-726-53 Sequence 53, Appl
38 4939 99.9 4077 26 US-09-580-339B-1 Sequence 1, Appli
39 4939 99.9 4103 26 US-09-572-411-7294 Sequence 7294, App
40 4939 99.9 3671 41 US-10-126-052A-7 Sequence 7, Appli
41 4935 99.9 3671 41 US-10-240-425-360 Sequence 360, App
42 4930 99.8 3604 53 US-10-643-795A-13 Sequence 13, Appl
43 4930 99.8 3604 63 US-10-948-518-13 Sequence 13, Appl
44 4930 99.8 3190 3 PCT-US99-04703-3 Sequence 3, Appli
45 4921 99.6 3190 3 PCT-US99-04703-3 Sequence 3, Appli

ALIGNMENTS

PCT-US01-47576-160
; Sequence 160, Application PC/TUS0147576
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tongtong
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Li, Samuel X.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Peckman, David W.
; APPLICANT: Cai, Feng
; APPLICANT: Fov, Teresa M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.45503PC
; CURRENT PUBLICATION NUMBER: PCT/US01/47576
; CURRENT PUBLICATION DATE: 2001-11-30
; PCT/US01-47576-160
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GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 18:32:20 ; Search time 469 Seconds

(without alignments)

5635.293 Million cell updates/sec

Title: US-10-623-155-161

Perfect score: 4942

Sequence: 1 WTQSRSTAGPICNLKFTVLIV.....HTLSRKRADKKNCTKLL 943

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 4791040

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-MAXLEN=200000000 -HOST=abs804

-USER=US10623155 @CN 1 1 255 @runat 13102006 101942 9842 -NCPU=6 -ICPU=3

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Database : Published Applications NA New.\*

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2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*

3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4939	99.9	2832	8	US-11-302-678-30 Sequence 30, Appl
2	4939	99.9	2970	8	US-11-302-678-28 Sequence 28, Appl
3	4939	99.9	4007	7	US-11-363-149-13 Sequence 13, Appl
4	4939	99.9	4007	7	US-11-363-151-13 Sequence 13, Appl
5	4388	88.8	2527	8	US-11-266-748A-184797 Sequence 184797,
6	1993	40.3	3311	6	US-10-700-439-87 Sequence 87, Appl
7	1965.5	39.8	3265	6	US-10-196-749-257 Sequence 257, Appl

8	1965.5	39.8	3265	8	US-11-101-316-69	Sequence 69, Appl
9	1965.5	39.8	3265	9	US-11-376-673-69	Sequence 69, Appl
10	1964.5	39.8	3204	8	US-11-302-678-31	Sequence 31, Appl
11	1964.5	39.8	3218	6	US-10-700-439-53	Sequence 53, Appl
12	1964.5	39.8	3218	8	US-11-266-748A-57517	Sequence 57517, A
13	1949.5	39.4	2754	8	US-11-302-678-33	Sequence 33, Appl
14	1880	38.0	1159	8	US-11-266-748A-184799	Sequence 184799,
15	1880	38.0	1159	8	US-11-266-748A-192237	Sequence 192237,
16	1403	28.4	1799	8	US-11-266-748A-184798	Sequence 184798,
17	1403	28.4	1799	8	US-11-266-748A-192296	Sequence 192296,
18	1040.5	21.1	1706	8	US-11-266-748A-4307	Sequence 4307, Ap
19	512.5	10.4	715	8	US-11-266-748A-5233	Sequence 5233, Ap
20	470	9.5	653	7	US-11-374-388-1851	Sequence 1851, Ap
21	468.5	9.5	533	7	US-11-374-388-1883	Sequence 1883, Ap
22	443.5	9.0	1000	8	US-11-266-748A-284991	Sequence 284991,
23	443.5	9.0	1000	8	US-11-266-748A-336420	Sequence 336420,
24	443.5	9.0	1000	8	US-11-266-748A-395149	Sequence 395149,
25	443.5	9.0	1000	8	US-11-266-748A-466195	Sequence 466195,
26	418	8.5	566	6	US-10-488-619-2714	Sequence 2714, Ap
27	357	7.2	1000	8	US-11-266-748A-222051	Sequence 222051,
28	357	7.2	1000	8	US-11-266-748A-287801	Sequence 287801,
29	357	7.2	1000	8	US-11-266-748A-339230	Sequence 339230,
30	357	7.2	1000	8	US-11-266-748A-398572	Sequence 398572,
31	357	7.2	1000	8	US-11-266-748A-469618	Sequence 469618,
32	327.5	6.6	833	8	US-11-266-748A-249419	Sequence 249419,
33	323.5	6.5	598	8	US-11-266-748A-5132	Sequence 5132, Ap
34	323.5	6.5	598	8	US-11-266-748A-63371	Sequence 63371, A
35	323.5	6.5	598	8	US-11-266-748A-66203	Sequence 66203, A
36	204	4.1	1000	8	US-11-266-748A-286631	Sequence 286631,
37	204	4.1	1000	8	US-11-266-748A-338060	Sequence 338060,
38	204	4.1	1000	8	US-11-266-748A-397144	Sequence 397144,
39	204	4.1	1000	8	US-11-266-748A-468190	Sequence 468190,
40	161.5	3.3	280	7	US-11-374-388-1868	Sequence 1868, Ap
41	154.5	3.1	432	7	US-11-190-172-2789	Sequence 2789, Ap
42	143.5	2.9	11784	8	US-11-266-748A-56711	Sequence 56711, A
43	134	2.7	3747	9	US-11-058-355B-91162	Sequence 91162, A
44	134	2.7	3747	9	US-11-056-355B-94918	Sequence 94918, A
45	130	2.6	4578	6	US-10-669-920-757	Sequence 757, App

#### ALIGNMENTS

#### RESULT 1

US-11-302-678-30  
; Sequence 30, Application US/11302678  
; Publication No. US2006008881A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641 260, 55089, 21407, 42032, 46556, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012P1RNM OMNI  
; CURRENT APPLICATION NUMBER: US/11/302.678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 18:21:41 ; Search time 2578 Seconds  
(without alignments)  
6741.994 Million cell updates/sec

Title: US-10-623-155-161  
Perfect score: 4942  
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Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 18992170 seqs, 6143817638 residues  
Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
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16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match Length	ID	Description
1	4942	100.0	3951	3 US-09-735-705-160 Sequence 160, App

2	4942	100.0	3951	3 US-09-850-716A-160 Sequence 160, App
3	4942	100.0	3951	3 US-09-897-778-160 Sequence 160, App
4	4942	100.0	3951	3 US-09-466-396A-160 Sequence 160, App
5	4942	100.0	3951	7 US-10-007-700-160 Sequence 160, App
6	4942	100.0	3951	7 US-10-117-982-160 Sequence 160, App
7	4942	100.0	3951	9 US-10-313-986-160 Sequence 160, App
8	4942	100.0	3951	10 US-10-775-972-160 Sequence 160, App
9	4942	100.0	3951	10 US-10-922-124-160 Sequence 160, App
10	4942	100.0	3951	10 US-10-623-155-160 Sequence 160, App
11	4939	99.9	2832	7 US-10-345-680-30 Sequence 30, Appl
12	4939	99.9	2970	6 US-10-055-412B-31 Sequence 31, Appl
13	4939	99.9	2970	7 US-10-345-680-28 Sequence 28, Appl
14	4939	99.9	2970	9 US-10-779-949-31 Sequence 31, Appl
15	4939	99.9	3671	7 US-10-295-027-317 Sequence 317, App
16	4939	99.9	3671	7 US-10-295-027-317 Sequence 1025, Ap
17	4939	99.9	3671	8 US-10-188-832-196 Sequence 196, App
18	4930	99.8	3604	8 US-10-240-425-360 Sequence 360, App
19	4930	99.8	3604	9 US-10-643-795A-13 Sequence 13, Appl
20	4930	99.8	3604	10 US-10-948-518-13 Sequence 13, Appl
21	4921	99.6	3190	6 US-10-270-595-3 Sequence 3, Appl
22	4921	99.6	3190	9 US-10-772-437-3 Sequence 3, Appl
23	4898.5	99.1	3156	3 US-09-919-172-86 Sequence 86, Appl
24	4898.5	99.1	3156	3 US-09-974-298-70 Sequence 70, Appl
25	4898.5	99.1	3156	9 US-10-752-986-86 Sequence 86, Appl
26	4790	96.9	2773	3 US-09-735-705-358 Sequence 358, App
27	4790	96.9	2773	3 US-09-850-716A-358 Sequence 358, App
28	4790	96.9	2773	3 US-09-897-778-358 Sequence 358, App
29	4790	96.9	2773	6 US-10-007-700-358 Sequence 358, App
30	4790	96.9	2773	7 US-10-117-982-358 Sequence 358, App
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33	4790	96.9	2773	10 US-10-922-124-358 Sequence 358, App
34	4790	96.9	2773	10 US-10-623-155-358 Sequence 358, App
35	4790	96.9	8031	3 US-09-735-705-254 Sequence 254, App
36	4790	96.9	8031	3 US-09-850-716A-254 Sequence 254, App
37	4790	96.9	8031	3 US-09-897-778-254 Sequence 254, App
38	4790	96.9	8031	6 US-10-007-700-254 Sequence 254, App
39	4790	96.9	8031	7 US-10-117-982-254 Sequence 254, App
40	4790	96.9	8031	7 US-10-313-986-254 Sequence 254, App
41	4790	96.9	8031	9 US-10-775-972-254 Sequence 254, App
42	4790	96.9	8031	10 US-10-922-124-254 Sequence 254, App
43	4790	96.9	8031	10 US-10-623-155-254 Sequence 254, App
44	4707.5	95.3	2784	3 US-09-735-705-168 Sequence 168, App
45	4707.5	95.3	2784	3 US-09-850-716A-168 Sequence 168, App

## ALIGNMENTS

RESULT 1  
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; Sequence 160, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 160

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 17:22:53 ; Search time 411 Seconds

(without alignments)  
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Perfect score: 4942

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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9	4942	100.0	3951	3	US-09-385-479-160	Sequence 160, App
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11	4939	99.9	2970	3	US-09-193-562B-31	Sequence 31, Appl
12	4939	99.9	2970	3	US-10-055-412B-31	Sequence 31, Appl
13	4921	99.6	3190	3	US-09-623-624-3	Sequence 3, Appli
14	4921	99.6	3190	3	US-10-270-595-3	Sequence 3, Appli
15	4908	99.3	3669	3	US-09-949-016-2224	Sequence 2224, Ap
16	4908	99.1	3156	3	US-09-919-172-86	Sequence 86, Appl
17	4790	96.9	2773	3	US-09-643-597-358	Sequence 358, App
18	4790	96.9	2773	3	US-09-630-940B-358	Sequence 358, App
19	4790	96.9	2773	3	US-10-007-700-358	Sequence 358, App
20	4790	96.9	8031	3	US-09-643-597-254	Sequence 254, App
21	4790	96.9	8031	3	US-09-480-884A-254	Sequence 254, App
22	4790	96.9	8031	3	US-09-542-615A-254	Sequence 254, App
23	4790	96.9	8031	3	US-09-606-421B-254	Sequence 254, App
24	4790	96.9	8031	3	US-09-476-496A-254	Sequence 254, App
25	4790	96.9	8031	3	US-09-630-940B-254	Sequence 254, App
26	4790	96.9	8031	3	US-10-007-700-254	Sequence 254, App
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28	4707.5	95.3	2784	3	US-09-480-884A-168	Sequence 168, App
29	4707.5	95.3	2784	3	US-09-542-615A-168	Sequence 168, App
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31	4707.5	95.3	2784	3	US-09-476-496A-168	Sequence 168, App
32	4707.5	95.3	2784	3	US-09-630-940B-168	Sequence 168, App
33	4707.5	95.3	2784	3	US-09-643-597-168	Sequence 168, App
34	4707.5	95.3	2784	3	US-09-480-884A-168	Sequence 168, App
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36	4596	78.3	2646	3	US-09-606-421B-431	Sequence 431, App
37	3869	78.3	3362	3	US-09-643-597-167	Sequence 167, App
38	3869	78.3	3362	3	US-09-480-884A-167	Sequence 167, App
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43	3869	78.3	3362	3	US-09-285-479-167	Sequence 167, App
44	3869	78.3	3362	3	US-09-285-479-167	Sequence 167, App
45	3869	78.3	3362	3	US-10-007-700-167	Sequence 167, App

#### ALIGNMENTS

RESULT 1

US-09-643-597-160  
; Sequence 160, Application US/096433597  
; Patent No. 6426072  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C11  
; CURRENT APPLICATION NUMBER: US/09/643,597  
; CURRENT FILING DATE: 2000-08-21  
; NUMBER OF SEQ ID NOS: 369  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 160  
; LENGTH: 3951  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-643-597-160

Alignment Scores: 0  
Pred. No.: 4942.00  
Score: Length: 3951  
Matches: 943

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2006, 16:55:05 ; Search time 843 Seconds  
(without alignments)  
10366.730 Million cell updates/sec

Title: US-10-623-155-160  
Perfect score: 3951  
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Post-processing: Minimum Match 0%  
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- 3: /EMC\_Celerra\_SID33/ptodata/1/pna/US07\_NEW\_COMB.seq.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	3928	99.4	4022	1	PCT-US06-33148-1639
5	3861	97.7	3955	1	PCT-US06-33148-1637
6	3861	97.7	3955	8	US-11-431-708-4126
7	3861	97.7	3955	8	US-11-475-062-7433
8	3613.2	91.5	3669	6	US-10-533-069-578
9	2827.8	71.6	2832	8	US-11-371-354-64288
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13	634.4	16.1	3195	6	US-10-276-115A-22
14	552.2	14.0	3350	8	US-11-475-062-9462
15	550.6	13.9	2804	1	PCT-US06-33148-1649
16	550.6	13.9	3311	1	PCT-US06-33148-23
17	550.6	13.9	3311	8	US-11-475-062-9463
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19	550.6	13.9	3340	1	PCT-US06-33148-1645
20	494.2	12.5	552	8	US-11-290-215A-172
21	462.4	11.7	2663	1	PCT-US06-33148-1647
22	449.4	11.4	451	8	US-11-290-215A-174
23	448.8	11.4	452	8	US-11-290-215A-370
24	434	11.0	4569	6	US-10-276-115A-3

25	319.6	8.1	731	8	US-11-433-832-31868	Sequence 31868, A
26	168.2	4.3	173	8	US-11-290-215A-173	Sequence 173, App
27	123.2	3.1	2350	8	US-11-433-832-31627	Sequence 31627, A
28	102	2.6	421	6	US-10-664-025A-2831	Sequence 2831, Ap
29	64	1.6	64	8	US-11-511-035-58690	Sequence 58690, A
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35	64	1.6	64	8	US-11-511-035-292067	Sequence 292067, A
36	64	1.6	64	8	US-11-511-035-314499	Sequence 314499, A
37	64	1.6	64	8	US-11-511-035-338355	Sequence 338355, A
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44	62	1.6	62	8	US-11-418-718-8647	Sequence 8647, Ap
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#### ALIGNMENTS

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; Sequence 1, Application US/10550797  
; GENERAL INFORMATION:  
; APPLICANT: Zehentner-Wilkinson, Barbara K.  
; APPLICANT: Hayes, Dawn  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION  
; FILE REFERENCE: 210121.60USPC  
; CURRENT APPLICATION NUMBER: US/10/550,797  
; CURRENT FILING DATE: 2005-09-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Corixa Invention Disclosure Database  
; SEQ ID NO 1  
; LENGTH: 3951  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-550-797-1

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Db	301	TACCAAGAGAGAGTATTTTTCAGNAATATAAGATTTTAACTCTGCCACATGGAAGC	360	



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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on:      October 13, 2006, 16:16:24 ; Search time 18707 Seconds
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Perfect score: 3951
Sequence: 1 tcgcgaccctattgaaaac.....taattaaaaaacataaaaaa 3951

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match		Length	DB	ID	Description
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6	3951	100.0	3951	28	US-09-685-696-160	Sequence 160, App	
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8	3951	100.0	3951	32	US-09-850-716-160	Sequence 160, App	
9	3951	100.0	3951	32	US-09-850-716A-160	Sequence 160, App	
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11	3951	100.0	3951	41	US-10-117-982-160	Sequence 160, App	
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13	3951	100.0	3951	52	US-10-623-155-160	Sequence 160, App	
14	3951	100.0	3951	60	US-10-775-972-160	Sequence 160, App	
15	3951	100.0	3951	62	US-10-923-124-160	Sequence 160, App	
16	3951	100.0	3951	74	US-11-392-479-1	Sequence 160, App	
17	3939.8	99.7	4007	74	US-11-363-149-13	Sequence 1, Appli	
18	3939.8	99.7	4007	75	US-11-363-151-13	Sequence 13, Appl	
19	3939.8	99.7	4007	84	US-60-679-970-1191	Sequence 13, Appl	
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21	3868.6	97.9	3944	79	US-60-213-360-3512	Sequence 3512, Ap	Qy	61	GAGGCTTCTCTCAACATGACCCAAAGAGGAGCATTCAGGTCCTATTATTCGAACCTGAAGTT	120
22	3861	97.7	3955	85	US-60-679-970-1190	Sequence 1190, Ap	Db	61	GAGGCTTCTCTCAACATGACCCAAAGAGGAGCATTCAGGTCCTATTATTCGAACCTGAAGTT	120
23	3834.4	97.0	4103	26	US-09-572-411-7294	Sequence 7294, Ap	Qy	121	TGTGACTCTCTGGTTCCTTAAGTTTCAAGAACTCCCAATTCCTGGGAGCTGGAGTACAGCT	180
24	3616.4	91.5	3669	41	US-10-170-235-25355	Sequence 25355, A	Db	121	TGTGACTCTCTGGTTCCTTAAGTTTCAAGAACTCCCAATTCCTGGGAGCTGGAGTACAGCT	180
25	3616.4	91.5	3669	62	US-10-940-774-2224	Sequence 2224, Ap	Qy	181	TCAAGCAATGGGTATTAATGGATTGCTCATTTGCAATTAATCTCAGGTACCTGAGAATCA	240
26	3616.4	91.5	3669	63	US-10-940-774A-2224	Sequence 2224, Ap	Db	181	TCAAGCAATGGGTATTAATGGATTGCTCATTTGCAATTAATCTCAGGTACCTGAGAATCA	240
27	3615.6	91.5	3669	82	US-60-453-050-531	Sequence 531, App	Qy	241	GAACCTCATCTCAACATTAAGAAATGATTAAGTAACTGAAAGCTTCAATTTTAAATGTC	300
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30	3613.2	91.5	3669	61	US-10-529-348-615	Sequence 615, App	Db	301	TACCAAGAGAAGAGTATTTTTCAGAAATATATAAGATTTTAACTCTGACCAATGGAAGC	360
31	3613.2	91.5	3669	61	US-10-821-801-70	Sequence 70, Appl	Qy	361	TAATAATAACAGCAAAATATAAGATTTTAACTCTGACCAATGGAAGC	420
32	3578.8	90.6	4077	26	US-09-580-339B-1	Sequence 1, Appl	Db	421	CTGCTATGGGCAATGGAGATGATCCATACACCTTACATACAGAGGCTGGAAGA	480
33	3547.2	89.8	3671	1	PCT-US02-21338A-196	Sequence 196, App	Qy	481	GGGAAATATACATTTTCAACCTTACTGATGATTAATCTGATTAATCTGATTAATCTGAT	540
34	3547.2	89.8	3671	1	PCT-US02-21338A-196	Sequence 196, App	Db	481	GGGAAATATACATTTTCAACCTTACTGATGATTAATCTGATTAATCTGATTAATCTGAT	540
35	3547.2	89.8	3671	41	US-10-126-052A-518	Sequence 518, App	Qy	541	CGGATCAGAGGCGAGTGTTCATGAAATGGGCGCACCTCCCTGGGCTGTTTGA	600
36	3547.2	89.8	3671	41	US-10-188-832-196	Sequence 196, App	Db	541	CGGATCAGAGGCGAGTGTTCATGAAATGGGCGCACCTCCCTGGGCTGTTTGA	600
37	3547.2	89.8	3671	43	US-10-295-027-317	Sequence 317, App	Qy	601	TGAGTATTAACATGACCAAACTTTTCTACATAAATGGGCGCAAAATCAATTAAGTGAAG	660
38	3547.2	89.8	3671	43	US-10-295-027-317	Sequence 317, App	Db	601	TGAGTATTAACATGACCAAACTTTTCTACATAAATGGGCGCAAAATCAATTAAGTGAAG	660
39	3547.2	89.8	3671	63	US-10-952-698-196	Sequence 196, App	Qy	661	GTGTTTCATCTGACATCAGGCAATTTTGTGTGTAAGAAAGGTCCTTGTGCTGCTGCTG	720
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42	3507	88.8	3604	53	US-10-643-795A-13	Sequence 13, Appl	Db	721	CTGTATTATTAGTAAGCTTTTAAAGAAAGGATGACCTTTATCTACAAATAGCAACCAAAA	780
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44	3104.4	78.6	3156	21	US-09-208-821-6	Sequence 6, Appl	Db	781	TGCAACTGCATCAATATGTTTCATGCAAGTTTATCTTCTGCTGCTGCTGCTGCTGCTG	840
45	3104.4	78.6	3156	31	US-09-786-133-27	Sequence 27, Appl	Qy	841	AAGTACCACCAACCAAGAGCACCACCACTTACAGAACAGATGTCAGGCTCAGAGTGC	900
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							Db	901	ATGGGATGTAATCAGACACTCTGCTGACTTTTCAACAGCTTTTCCCAATGAAACGGGACTGA	960
							Qy	961	GCTTCCACCTTCCCAATGTTTGTGTAAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGT	1020
							Db	961	GCTTCCACCTTCCCAATGTTTGTGTAAGGCTGTTGAGAGGCTGTTGAGAGGCTGTTGAGT	1020
							Qy	1021	GCTGATGTGTCAGCAAGATGTCAGAGGCTGACAGACTCTTCAACTACAAACAGCGC	1080
							Db	1021	GCTGATGTGTCAGCAAGATGTCAGAGGCTGACAGACTCTTCAACTACAAACAGCGC	1080
							Qy	1081	AGAAATTTTATGATGAGATTTGTTGAAATTCATACCTTCGTGGGCAATTCGCGATTCGA	1140
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							Qy	1141	CAGCAAGAGGAGATCAGAGCCAGCTACACCAATTAACAGCAATGATGATCGAAGTT	1200

# ALIGNMENTS

RESULT 1

PCT-US01-47576-160

; Sequence 160, Application PC/TUS0147576

; GENERAL INFORMATION:

; APPLICANT: Corixa Corporation

; APPLICANT: Wang, Tongtong

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Li, Samuel X.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Fanger, Neil

; APPLICANT: Retter, Marc W.

; APPLICANT: Durham, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedwick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Peckman, David W.

; APPLICANT: Cai, Feng

; APPLICANT: Foy, Teresa M.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.45503PC

; CURRENT APPLICATION NUMBER: PCT/US01/47576

; CURRENT FILING DATE: 2001-11-30

; NUMBER OF SEQ ID NOS: 469

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 160

; LENGTH: 3951

; TYPE: DNA

; ORGANISM: Homo sapiens

PCT-US01-47576-160

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Matches 3951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1141 CAGCAAG  
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GenCore version 5.1.9  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2930	74.2	2970	8	US-11-302-678-28	Sequence 28, Appl
4	2827.2	71.6	2832	8	US-11-302-678-30	Sequence 30, Appl
5	2497.4	63.2	2527	8	US-11-266-748A-184797	Sequence 184797,
6	1748.6	44.3	1799	8	US-11-266-748A-184798	Sequence 184798,
7	1748.6	44.3	1799	8	US-11-266-748A-184799	Sequence 184799,
8	1138	28.8	1159	8	US-11-266-748A-184799	Sequence 184799,
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14	652.8	16.5	3204	8	US-11-302-678-31	Sequence 31, Appl
15	652.8	16.5	3218	8	US-10-700-439-53	Sequence 53, Appl
16	652.8	16.5	3218	8	US-11-266-748A-57517	Sequence 57517, A
17	646.8	16.4	3265	6	US-10-196-749-257	Sequence 257, App
18	646.8	16.4	3265	9	US-11-101-316-69	Sequence 69, Appl
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20	645.4	16.3	2754	8	US-11-302-678-33	Sequence 33, Appl
21	550.6	13.9	3311	6	US-10-700-439-87	Sequence 87, Appl
22	533.8	13.5	538	8	US-11-266-748A-82206	Sequence 82206, A
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24	308.2	7.8	1706	8	US-11-266-748A-4307	Sequence 4307, Ap
25	177	4.5	833	8	US-11-266-748A-249419	Sequence 249419,
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28	138.4	3.5	715	8	US-11-266-748A-5233	Sequence 5233, Ap
29	124	3.1	566	6	US-10-488-619-2714	Sequence 2714, Ap
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34	103.4	2.6	1000	8	US-11-266-748A-222051	Sequence 222051,
35	103.4	2.6	1000	8	US-11-266-748A-287801	Sequence 287801,
36	103.4	2.6	1000	8	US-11-266-748A-339230	Sequence 339230,
37	103.4	2.6	1000	8	US-11-266-748A-398572	Sequence 398572,
38	103.4	2.6	1000	8	US-11-266-748A-469618	Sequence 469618,
39	96	2.4	598	8	US-11-266-748A-5132	Sequence 5132, Ap
40	96	2.4	598	8	US-11-266-748A-63371	Sequence 63371, A
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ALIGNMENTS

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; Publication No. US20060194237A1  
; GENERAL INFORMATION:  
; APPLICANT: LATOV, NORMAN  
; TITLE OF INVENTION: METHODS FOR DIAGNOSING PERIPHERAL NEUROPATHY  
; FILE REFERENCE: 67366-228224  
; CURRENT APPLICATION NUMBER: US/11/363.149  
; CURRENT FILING DATE: 2006-02-28  
; PRIOR APPLICATION NUMBER: 60/657,122  
; PRIOR FILING DATE: 2005-02-28  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: Patent In Ver. 3.3  
; SEQ ID NO 13  
; LENGTH: 4007  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-11-363-149-13

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	3951	100.0	3951	3	US-09-466-396A-160
5	3951	100.0	3951	6	US-10-007-700-160
6	3951	100.0	3951	7	US-10-117-982-160
7	3951	100.0	3951	7	US-10-313-986-160
8	3951	100.0	3951	9	US-10-775-972-160
9	3951	100.0	3951	10	US-10-922-124-160
10	3951	100.0	3951	10	US-10-623-155-160
11	3547.2	89.8	3671	7	US-10-295-027-317
12	3547.2	89.8	3671	7	US-10-295-027-317
13	3547.2	89.8	3671	8	US-10-188-832-136
14	3507	88.8	3604	8	US-10-240-425-360
15	3507	88.8	3604	9	US-10-643-795A-13
16	3507	88.8	3604	10	US-10-948-518-13
17	3104.4	78.6	3156	3	US-09-919-172-86

18	3104.4	78.6	3156	3	US-09-974-298-70	Sequence 70, Appl
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20	3101.2	78.5	3190	6	US-10-270-595-3	Sequence 3, Appl
21	3101.2	78.5	3190	9	US-10-772-437-3	Sequence 3, Appl
22	2930	74.2	2970	6	US-10-055-412B-31	Sequence 31, Appl
23	2930	74.2	2970	7	US-10-345-680-28	Sequence 28, Appl
24	2930	74.2	2970	7	US-10-779-949-31	Sequence 31, Appl
25	2827.2	71.6	2832	7	US-10-345-680-30	Sequence 30, Appl
26	2800.8	70.9	3362	3	US-09-735-705-167	Sequence 167, App
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36	2772	70.2	2784	3	US-09-735-705-168	Sequence 168, App
37	2772	70.2	2784	3	US-09-850-716A-168	Sequence 168, App
38	2772	70.2	2784	3	US-09-897-778-168	Sequence 168, App
39	2772	70.2	2784	3	US-09-466-396A-168	Sequence 168, App
40	2772	70.2	2784	6	US-10-007-700-168	Sequence 168, App
41	2772	70.2	2784	7	US-10-117-982-168	Sequence 168, App
42	2772	70.2	2784	7	US-10-313-986-168	Sequence 168, App
43	2772	70.2	2784	9	US-10-775-972-168	Sequence 168, App
44	2772	70.2	2784	10	US-10-922-124-168	Sequence 168, App
45	2772	70.2	2784	10	US-10-623-155-168	Sequence 168, App

## ALIGNMENTS

### RESULT 1

US-09-735-705-160  
; Sequence 160, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:

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APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 160

LENGTH: 3951

TYPE: DNA

ORGANISM: Homo sapien

US-09-735-705-160

Query Match 100.0%; Score 3951; DB 3; Length 3951;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TCTGCATCCATTGAAACCTGACACATGATGACAGGCTCAGTGTGAGTGAACCTG	60
Db	1	TCTGCATCCATTGAAACCTGACACATGATGACAGGCTCAGTGTGAGTGAACCTG	60
Qy	61	GAGGCTTCTCTACACATGACCCAAAGAGCATGAGGCTCTATTTCACACCTGAAGTT	120